

Figure 2 (page 1 of 2)

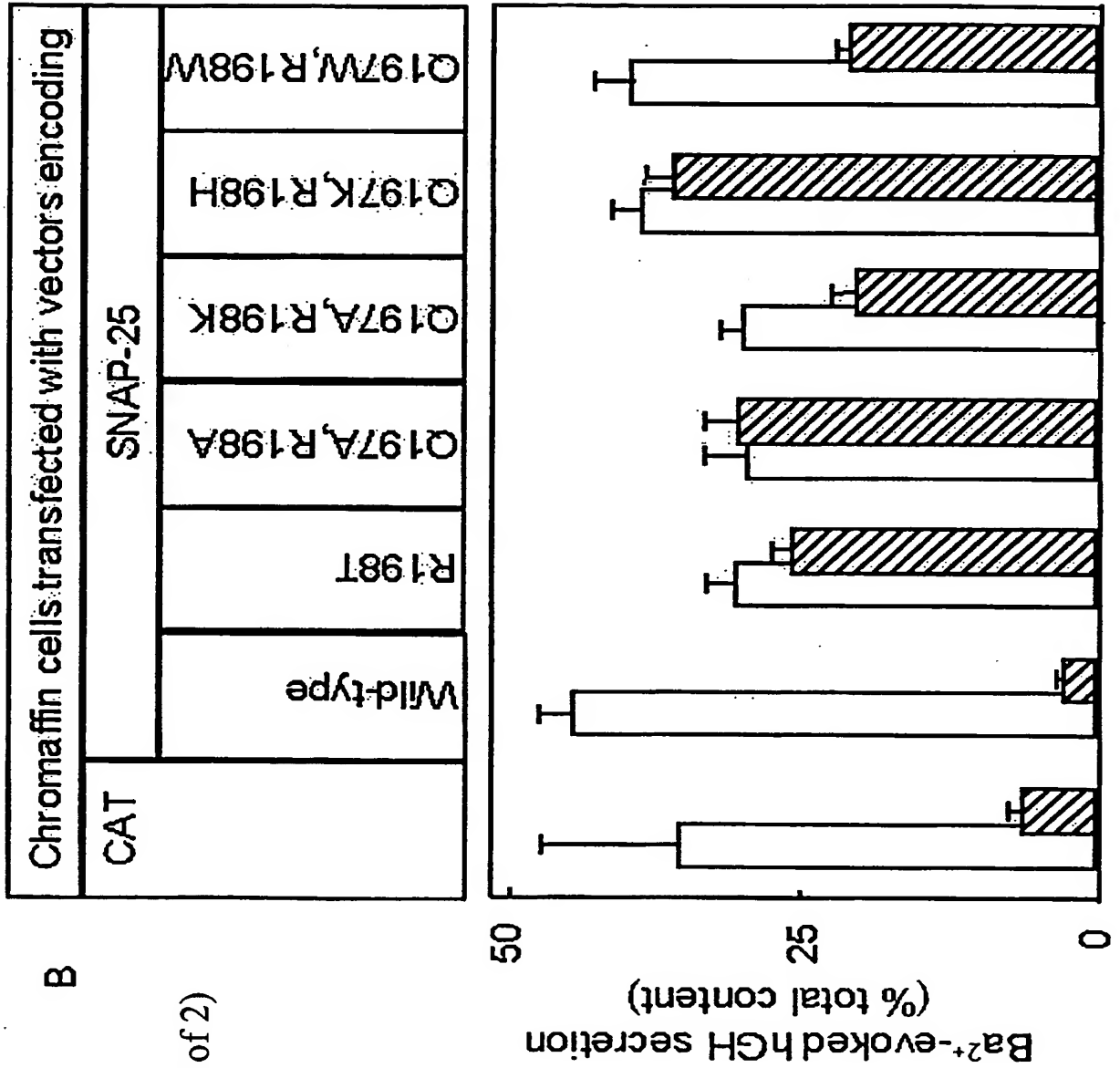
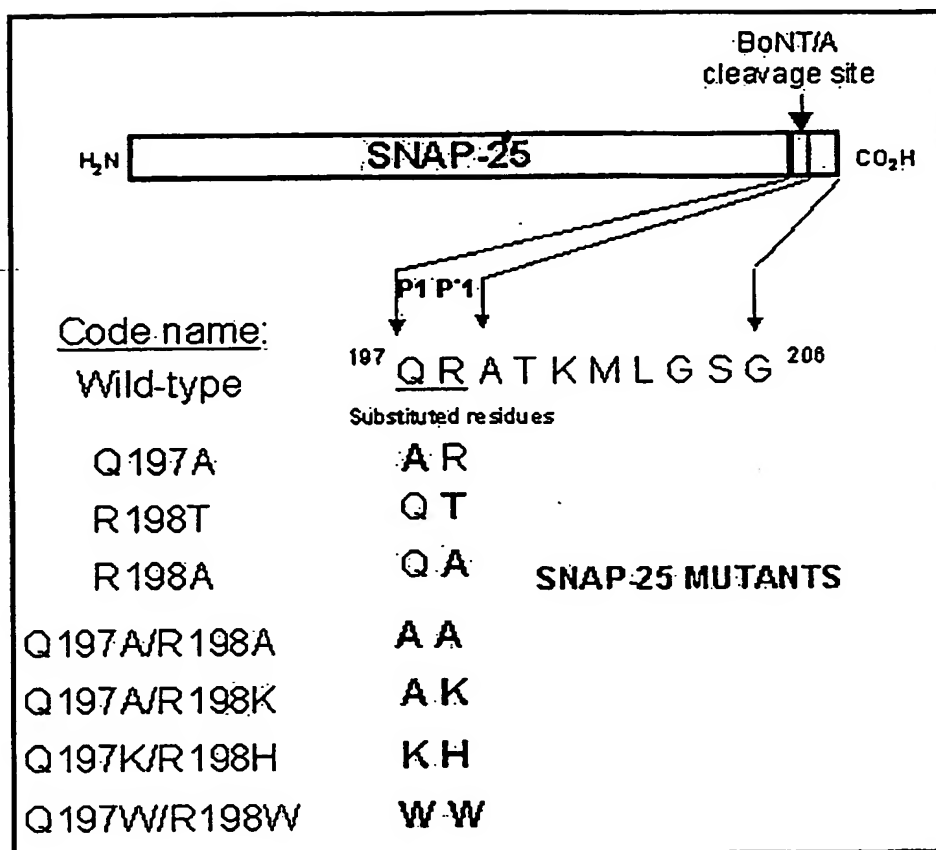


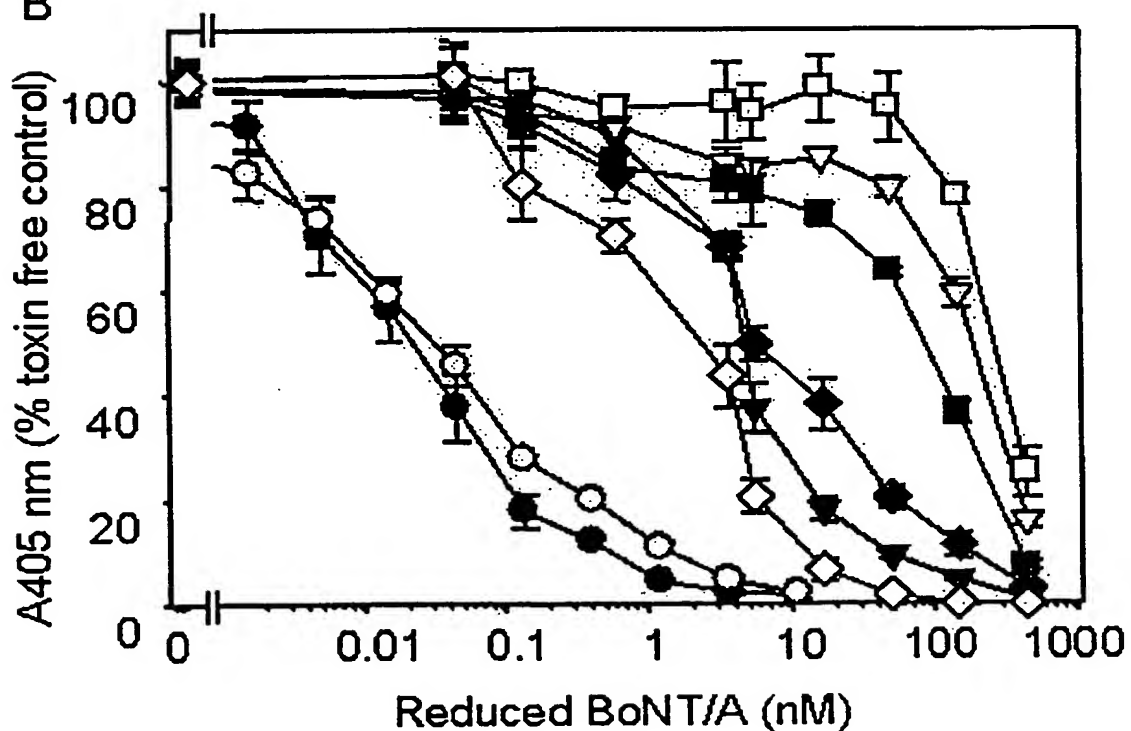
Figure 2 (page 2 of 2)

Figure 3

A



B



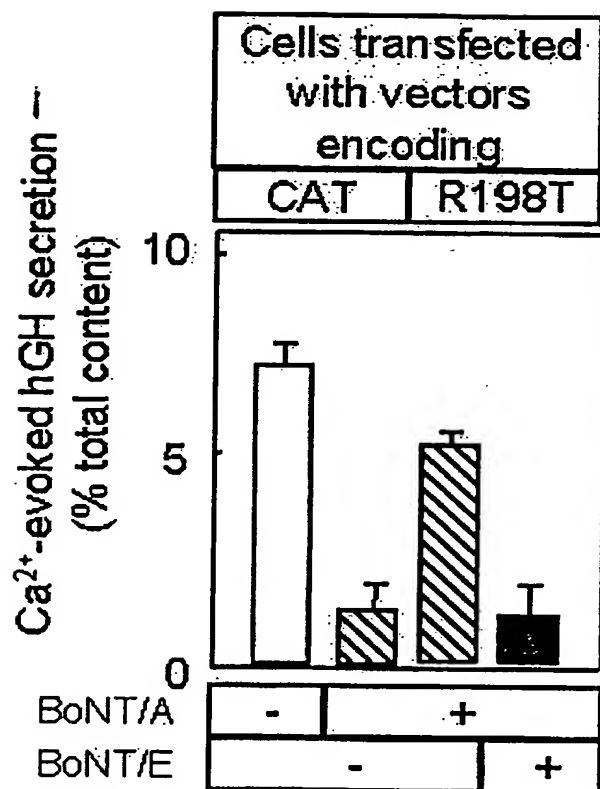


Figure 4

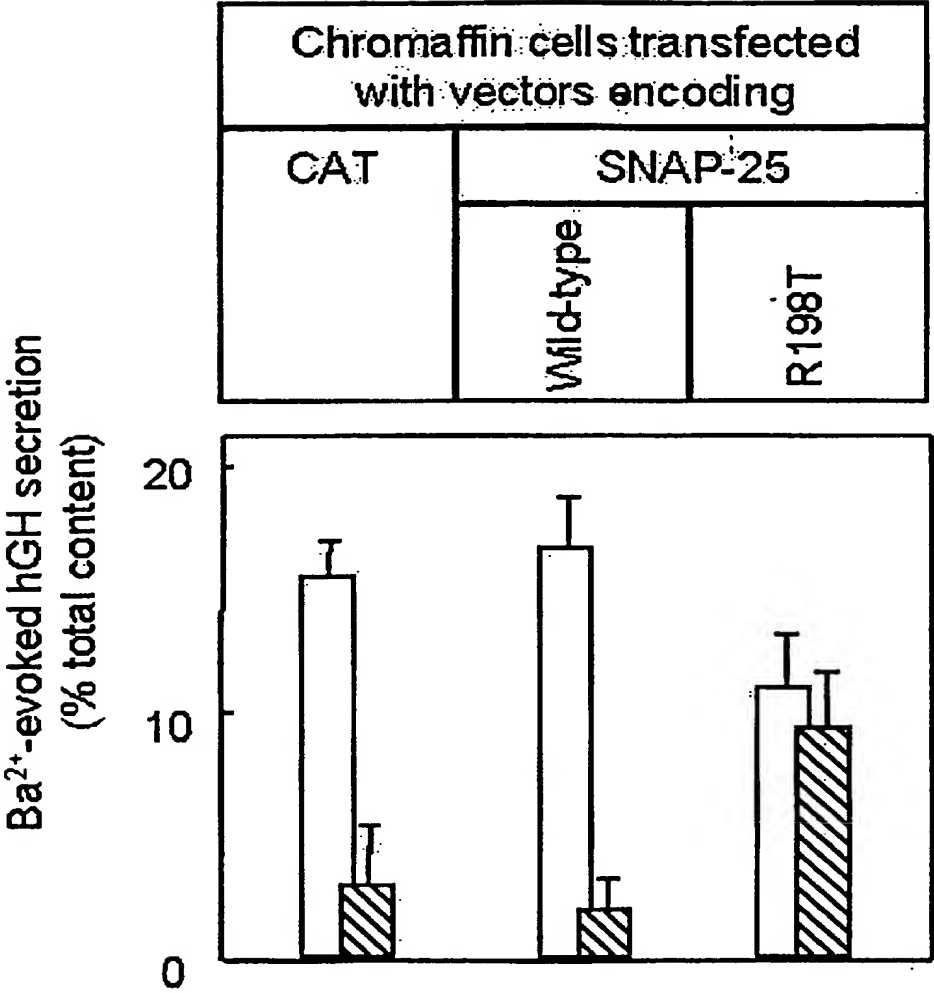


Figure 5

A

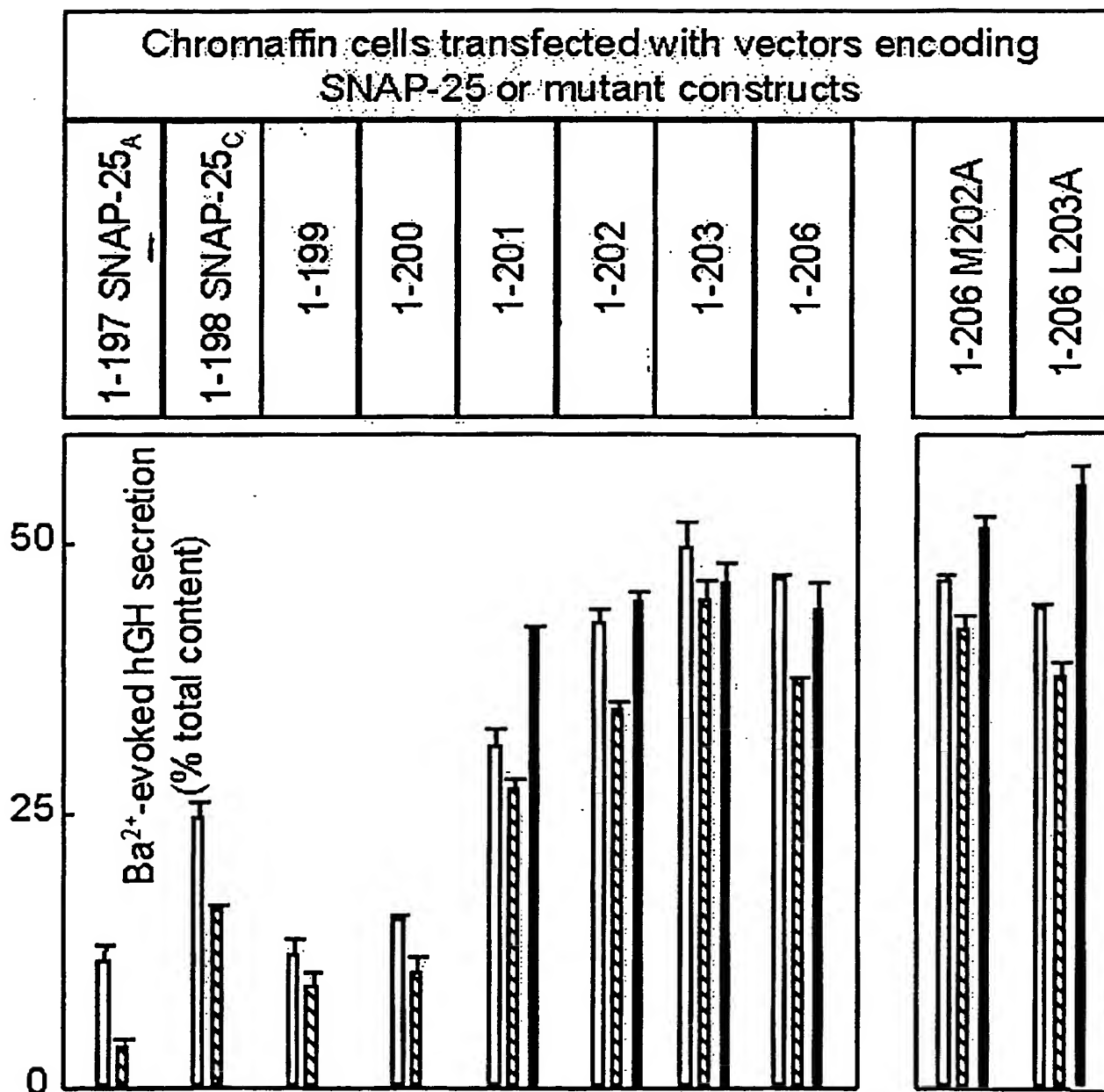


Figure 6 (page 1 of 2)

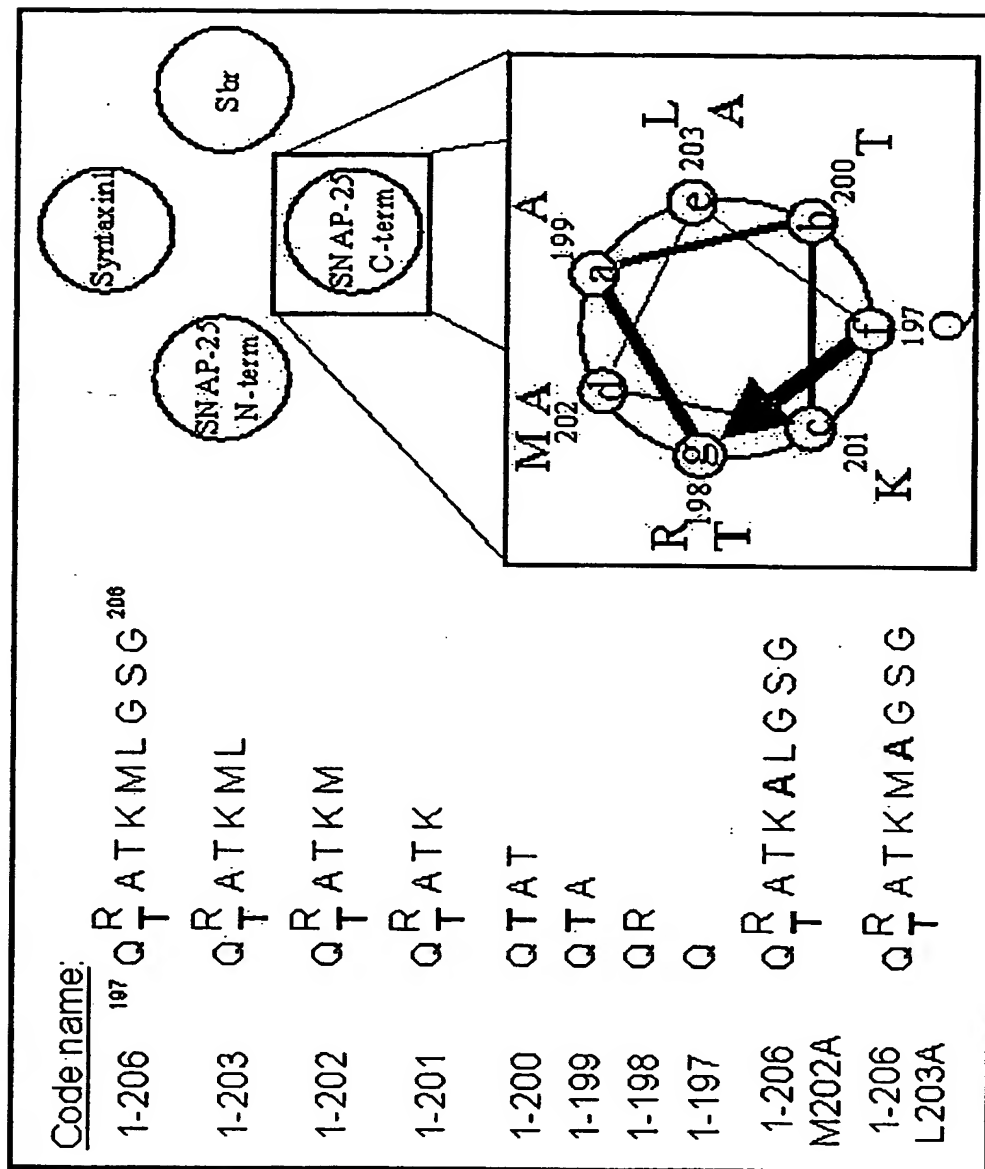


Figure 6 (page 2 of 2)

SNAP-25 145 - E M D E N L E Q V S G I I G N L R N M A L D M G N E I D T Q N R Q I
hSNAP-23 151 - E M E E N L T Q V G S I L G N L K D M A L N I G N E I D A Q N P Q I
mSNAP-23 150 - E M E E N L T Q V G S I L G N L K N M A L D M G N E I D A Q N Q Q I

: : : : :

BoNT/E BoNT/A C
 ↓ ↓ ↓
SNAP-25 179 - D R I M E K A D S N K T R I D E A N Q R A T K M L G S G - 206
hSNAP-23 185 - K R I T D K A D T N R R D R I D I A N A R A K K L I D S - 211
mSNAP-23 184 - Q K I T E K A D T N K N R I D I A N T R A K K L I D S - 210
: : : : :

MW

SNAP-25			hSNAP-23			mSNAP-23					
-	A	C	E	-	A	C	E	-	A	C	E

Figure 7

Figure 7



LOCUS HSVAMP1MR 354 bp mRNA PRI 17-FEB-1997
DEFINITION H.sapiens Vamp1 mRNA.
ACCESSION Z48924 VERSION Z48924.1 GI:758107

protein_id="CAA88760.1" /db_xref="GI:758108"
/db_xref="SWISS-PROT:P23763"
/translation="MSAPAQPPAEGTEGTAPGGGPPGPPPNMTSNRRRLQQT
QAQVEEVVDIIRVNVDKVLERDQKLSELDADRADALQAGASQFESSAAKLKR
KYWWKNCKMMIMLG TICAIIVVVIVIVYFFT"
BASE COUNT 96 a 82 c 103 g 73 t
ORIGIN
1 atgtctgctc cagctcagcc acctgctgaa gggacagaag
ggactgcccc aggtgggggt
61 ccccttgccc ctcctcctaa catgaccagt aacagacgac
ccagcaaac ccaggcacia
121 gtggaggagg tgggtggacat catacgtgtg aacgtggaca
aggtcctgga gagggaccag
181 aagctgtcag agctggatga ccgagctgat gccttgcagg
caggagcatc acaatttgag
241 agcagtgtg caaagctaaa gaggaagtat tgggtggaaaa
actgcaagat gatgatcatg
301 ctgggaacca tctgtgccat catcgtggta gttattgtaa
tctacttttt tact //

Figure 8 (page 1 of 11)

GenBank Acc: AI815549 GenBank gi: 5431095
IMAGE:2517969 (5')

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GCCATGTCTGCTACCGCTGCCACGGCCCCCCCCTGCTGCCCCGGCTGGGGAG
GGTGGTCCCCCTGCACCCCCTCCAAACCTCACCAGTAACAGGAGACTGCAG
CAGACCCAGGCCCCAGGTGGATGAGGTGGTGGACATCATGAGGGTGAACGTG
GACAAGGTCCTGGAGCGAGACCAGAAGCTGTCGGAGCTGGACGACCGTGCA
GATGCACTCCAGGCGGGGGCCTCCCAGTTTGAAACAAGCGCAGCCAAGCTC
AAGCGCAAATACTGGTGGAAAAACCTCAAGATGATGATCATCTTGGGAGTG
ATTTGCGCCATCATCCTCATCATCATCATAGTTTACTTCAGCACTTAAATC
CCCGAGGAGTCTGCCCTGCCTAGAGAAGGGCCTCTCCCCCAACCCTCAGCC
GTTCCCTCCACCTCTCAGCCAT ATCTNTCAGCCCCCCCCTC

Figure 8 (page 2 of 11)

11/21

EST name: ui73f02.y1 GenBank Acc:
AI785090 GenBank gi: 5332806 Clone Id:
IMAGE:1888059 (5')
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ACCCCCGCCATGTCGGCTACCGCTGCCACCGTCCCGCCTGCCGCCCCGGCC
GGCGAGGGTGGCCCCCCTGCACCTCCTCCAAACCTTACTAGTAACAGGAGA
CTGCAGCAGACCCAGGCCAGGTGGATGAGGTGAGTGTGTGTGTGTGTCTG
TGTCTGTGTCTATGTCTATGTATGTCAAAGATGCAAGATGATGGGCTGGCA
AATAGGTGTGGGAGCCCATCTTGGGTGAAGGTAAAGACAGCTTATGCTTG
TGGGTTTTGGTCGGAGACCTGCCTCAT

Figure 8 (page 3 of 11)

12/21

LOCUS NM_004781 638 bp mRNA PRI 27-JUN-2000
DEFINITION Homo sapiens vesicle-associated membrane
protein 3 (cellubrevin) (VAMP3), mRNA.
ACCESSION NM_004781 VERSION NM_004781.2 GI:9257252
protein_id="NP_004772.1" /db_xref="GI:4759300"
/translation="MSTGPTAATGSNRRLQQTQNQVDEVVDIMRVNVDKVL
ERDQKLS
ELDDRADALQAGASQFETSAAKLKRKYWWKNCKMWAIGITVLVIFIIIIIV
WVVS" BASE COUNT 181 a 133 c 141 g 183 t ORIGIN 1
ctctaaagcg ccgcagctgc caaaatgtct acaggtccaa
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aatcaagta gatgaggtgg tggacataat gcgagttaac 121
gtggacaagg ttctggaaag agaccagaag ctctctgagt
tagacgaccg tgcagacgca 181 ctgcaggcag gcgcttctca
at ttgaaacg agcgcagcca agttgaagag gaaatattgg 241
tggaagaatt gcaagatgtg ggcaatcggg attactgttc
tggttatctt catcatcatc 301 atcatcgtgt gggttgtctc
ttcatgaaga accagcggaa ctcaaaactg ctgttcaaga 361
aacctcttca agacttttga cttagaacct gctatattat
caagcttacc tactgttatc 421 tctaaaattt tttttgtgtt
aatgtaaagt tgaatttcta ggaaacgtgc ctttgttttt 481
taatatgcac tccaaattag aaggccggcc ccgtccacat
tttgcacagt gccttttacag 541 atttacgtat gggctgatga
agaggccttc ttaagttcca gagtgctata atctagatgt 601
aatgttgtca ctaattaatt gccattactc cccttttag //

Figure 8 (page 4 of 11)

LOCUS HSU55936 800 bp mRNA PRI 14-JUN-1996
 DEFINITION Human SNAP-23 mRNA, complete cds.
 ACCESSION U55936 VERSION U55936.1 GI:1374812
 SOURCE human.

protein_id="AAC50537.1" /db_xref="GI:1374813"

/translation="MDNLSSEEIQQRAHQITDESLESTRRILGLAIESQDA
 GIKTITMLDEQKEQLNRIEEGLDQINKDMRETEKLTLELNKCCGLCVCPCN
 RTKNFESGKAYKTTWGDGGENSPCNVVSQPGPVTNGQLQQPTTGAVSGGY
 IKRITNDAREDEMEENLTQVGSILGNLKDMLNIGNEIDAQNPQIKRITDK
 ADTNRDRIDIANARAKKLIDS"

BASE COUNT 266 a 167 c 192 g 175 t ORIGIN

```

1  ctcgaggcca cgaaggccgc caggtccggt gttgggggtgt
   ccgagttgcc gccggagagg 61 agtggcctcg cccgcttgag
   ttttgattca tcatggataa tctgtcatca gaagaaattc 121
   aacagagagc tcaccagatt actgatgagt ctctggaaag
   tacgaggaga atcctggggt 181 tagccattga gtctcaggat
   gcaggaatca agaccatcac tatgctggat gaacaaaagg 241
   aacaactaaa ccgcatagaa gaaggcttgg accaaataaa
   taaggacatg agagagacag 301 agaagacttt aacagaactc
   aacaaatgct gtggcctttg tgtctgccca tgtaatagaa 361
   caaagaactt tgagtctggc aaggcttata agacaacatg
   gggagatggt ggagaaaact 421 caccttgcaa tgtagtatct
   aaacagccag gcccggtgac aaatggtcag cttcagcaac 481
   caacaacagg agcagtcagt ggtggataca ttaaacgcat
   aactaatgat gccagagaag 541 atgaaatgga agagaacctg
   actcaagtgg gcagtatcct gggaaatcta aaagacatgg 601
   ccctgaacat aggcaatgag attgatgctc aaaatccaca
   aataaaaacga atcacagaca 661 aggctgacac caacagagat
   cgtattgata ttgccaatgc cagagcaaag aaactcattg 721
   acagctaaag ctactgctgt tcttctttat catttattca
   cttccgtagc tcctccttga 781 aagttattac cttttcagag

```

Figure 8 (page 5 of 11)

DEFINITION Human nerve-terminal protein (isoform SNAP25A) mRNA, complete cds.

ACCESSION L19760

VERSION L19760.1 GI:307425

SOURCE Homo sapiens cDNA to mRNA.

/protein_id="AAC37545.1"

/db_xref="GI:307426"

/translation="MAEDADMRNELEEMQRRADQLADESLESTRMLQLVE
ESKDAGIRTLVMLDEQGEQLDRVEEGMNHINQDMKEAEKNLKD LGKCCGLF
ICPCNKLKSSDAYKKAWGNNQDGVVASQPARVVDEREQMAISGGFIRRVTN
DARENEMDENLEQVSGIIGNLRHMA LDMGNEIDTQNRQIDRIMEKADS NKT
RIDEANQRATKMLGSG"

BASE COUNT 260 a 223 c 237 g 203 t
ORIGIN

1 aacacaaccc tcccgagaag cccaggtcca gagccaaacc
cgtcactgac cccccagccc
61 aggcgcccag ccactcccca ccgctaccat ggccgaagac
gcagacatgc gcaatgagct
121 ggaggagatg cagcgaaggg ctgaccagtt ggctgatgag
tcgctggaaa gcacccgtcg
181 tatgctgcaa ctggttgaag agagtaaaga tgctggtatc
aggactttgg ttatggttga
241 tgaacaagga gaacaactcg atcgtgtcga agaaggcatg
aaccatatca accaagacat
301 gaaggaggct gagaaaaatt taaaagattt agggaaatgc
tgtggccttt tcatatgtcc
361 ttgtaacaag cttaaatcaa gtgatgctta caaaaaagcc
tggggcaata atcaggatgg
421 agtggtggcc agccagcctg ctcgtgtagt ggacgaacgg
gagcagatgg ccatcagtgg
481 cggcttcatc cgcagggtta caaatgatgc ccgagaaaat
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541 gcaggtgagc ggcatcatcg ggaacctccg tcacatggcc
ctggatatgg gcaatgagat
601 cgatacacag aatcgccaga tcgacaggat catggagaag
gctgattcca acaaaaccag

Figure 8 (page 6 of 11)

661 aattgatgag gccaaccaac gtgcaacaaa gatgctggga
agtggttaag tgtgcccacc
721 cgtgttctcc tccaaatgct gtcgggcaag atagctcctt
catgcttttc tcatggtatt
781 atctagtagg tctgcacaca taacacacat cagtccaccc
ccattgtgaa tgttgtcctg
841 tgtcatctgt cagcttccca acaatacttt gtgtcttttg
ttctctcttg gtctctttct
901 ttccaaagggt tgtacatagt ggt
//

Figure 8 (page 7 of 11)

16/21

LOCUS HUMSNAP25B 923 bp mRNA PRI 25-MAR-1994
 DEFINITION Human nerve-terminal protein (isoform
 SNAP-25b) mRNA, complete cds.
 ACCESSION L19761 VERSION L19761.1 GI:307427

/protein_id="AAC37546.1" /db_xref="GI:307428"
 /translation="MAEDADMRNELEEMQRRADQLADESLESTRMLQOLVE
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 VCPCKLSSDAYKKAWGNNQDGVVASQPARVVDEREQMAISGGFIRRVTN
 DARENEMDENLEQVSGIIGNLRHMAIDMGNEIDTQNRQIDRIMEKADSNT
 RIDEANQRATKMLGSG"

BASE COUNT 260 a 223 c 243 g 197 t ORIGIN
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 ccgctaccat ggccgaagac gcagacatgc gcaatgagct 121
 ggaggagatg cagcgaaggg ctgaccagtt ggctgatgag
 tcgctggaaa gcacccgtcg 181 tatgctgcaa ctggttgaag
 agagtaaaga tgctggtatc aggactttgg ttatgttgga 241
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 gaccaaataca ataaggacat 301 gaaagaagca gaaaagaatt
 tgacggacct aggaaaattc tgcgggcttt gtgtgtgtcc 361
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 tggggcaata atcaggacgg 421 agtgggtggc agccagcctg
 ctcgtgtagt ggacgaacgg gagcagatgg ccatcagtgg 481
 cggcttcatc cgcagggtta caaatgatgc ccgagaaaat
 gaaatggatg aaaacctaga 541 gcaggtgagc ggcattcatc
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 taacacacat cagtccaccc ccattgtgaa tgttgctcctg 841
 tgtcatctgt cagcttccca acaatacttt gtgtctttttg
 ttctctcttg gtctctttct 901 ttccaaaggt tgtacatagt ggt

Figure 8 (page 8 of 11)

LOCUS HUMSYN1A 2088 bp mRNA PRI 28-NOV-1994
 DEFINITION Human syntaxin 1A mRNA, complete cds.
 ACCESSION L37792 VERSION L37792.1 GI:577487
 Swiss-Prot Accession Number P32851
 protein_id="AAA53519.1" /db_xref="GI:577488"
 /translation="MKDRTQELRTAKDSDDDDVAVTVDRDRFMDEFFEQV
 EEIRGFIDKIAENVVEEVKRKHSAILASPNPDEKTKEELEELMSDIKKTANK
 VRSKLKSIEQSIEQEEGLNRSSADLRIRKTQHSTLSRKFEVVMSEYNATQS
 DYRERCKGRIQRQLEITGRTTTSEELEDMLESGNPAIFASGIIMDSSISKQ
 ALSEIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVEHAV
 DYVERAVSDTKKAVKYQSKARRKKIMIIICCVILGIVIASTVGGIFA"

BASE COUNT 447 a 635 c 604 g 402 t ORIGIN
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 agcgatgatg atgatgatgt 61 cgctgtcacc gtggaccgag
 accgcttcat ggatgagttc tttgagcagg tggaggagat 121
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Figure 8 (page 9 of 11)

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ctgctcttcc ctggggaccc taacctcgcc tccagctgac
ctgccctgtc ctctccagct 1261 gtccccacaa gcagagccct
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Figure 8 (page 10 of 11)

	10	20	30	40	50
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MOUSES25. PRO MAEDADMNRNELEEMQRRADQLADESLESTRRLMLQLVEESKDAGIRTLVML					

HUMANS25.PRO DEQGEQLDRVEEGMNHINQDMKEAEKNLKDGLKCCGLFICPCNKLKSSDA
| | | | | : | | | | : | | | | | . | | | | | : | | | | | | | |
MOUSES25.PRO DEQGEQLERIEEGMDQINKDMKEAEKNLTDLGKFCLVCVCPCNKLKSSDA
60 70 80 90 100 60 70 80 90 100

	110	120	130	140	150					
HUMANS25.PRO	YKKA	GNQD	GVAS	QPAR	VDEREQ	MAISGG	FIRVT	DARE	NEMD	ENL
MOUSES25.PRO	YKKA	GNQD	GVAS	QPAR	VDEREQ	MAISGG	FIRVT	DARE	NEMD	ENL

	160	170	180	190	200
HUMANS25.PRO	EQVSGIIGNLRHMA	DMGNEIDTQNRQI	DRIMEKADSNKTR	IDEANQ	RAT
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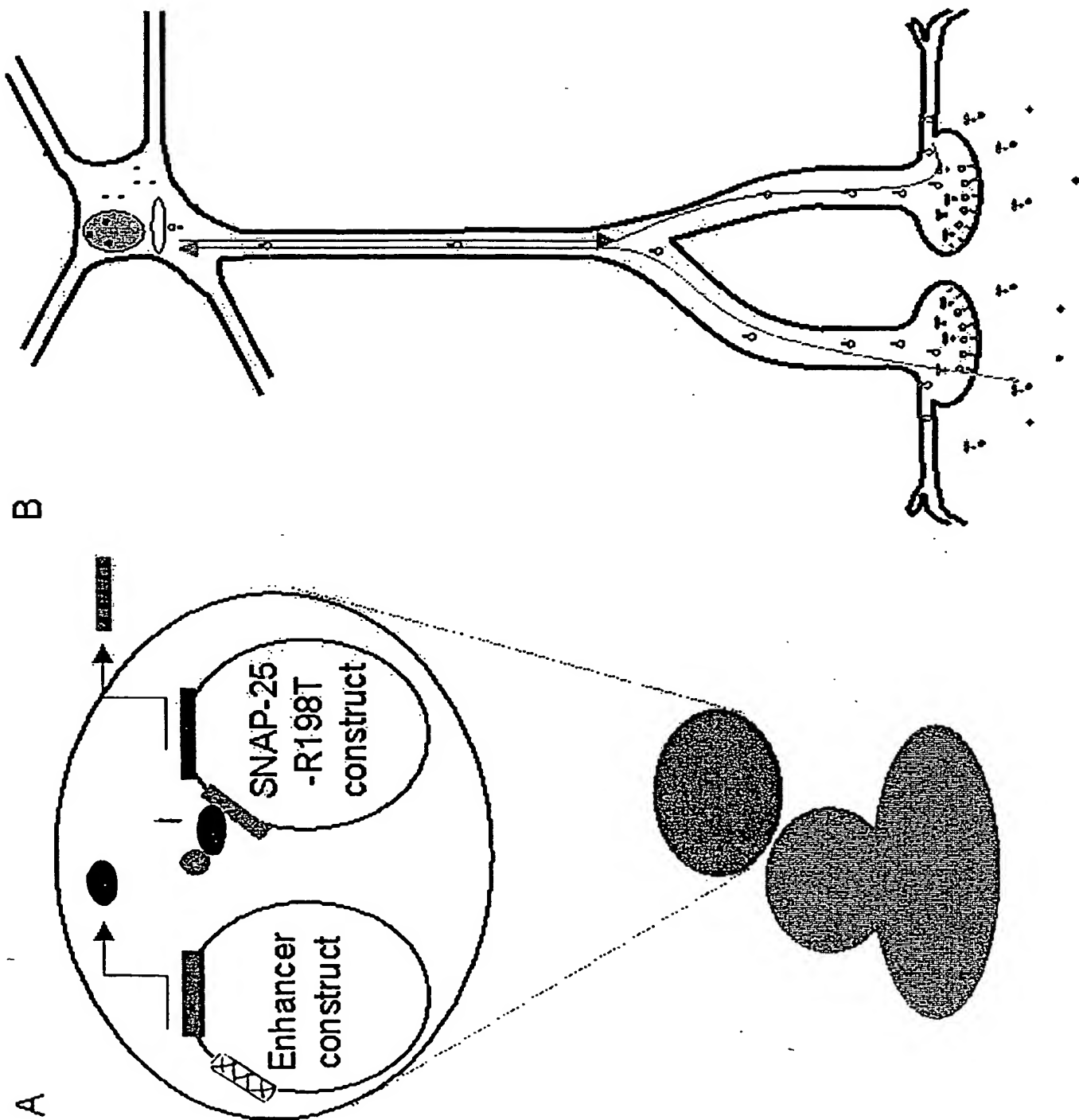
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HUMANS25.PRO  KMLGSG
                |||||
MOUSES25.PRO  KMLGSG

Lipman-Pearson Protein Alignment
Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12
Seq1(1>206) HUMANS25.PRO
Seq2(1>206) MOUSES25.PRO
Similarity Index 95.6 Gap Number 0 Gap Length 0
Consensus Length 206

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Figure 9



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